

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/594,732
Source: IFWP
Date Processed by STIC: 10/10/06

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 10/394,732

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- | | | |
|----|------------------------------------|---|
| 1 | Wrapped Nucleic
Wrapped Aminos | The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping." |
| 2 | Invalid Line Length | The rules require that a line not exceed 72 characters in length. This includes white spaces. |
| 3 | Misaligned Amino
Numbering | The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead. |
| 4 | Non-ASCII | The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text. |
| 5 | Variable Length | Sequence(s) ____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing. |
| 6 | PatentIn 2.0
"bug" | A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences. |
| 7 | Skipped Sequences
(OLD RULES) | Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped
Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences. |
| 8 | Skipped Sequences
(NEW RULES) | Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000 |
| 9 | Use of n's or Xaa's
(NEW RULES) | Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents. |
| 10 | Invalid <213>
Response | Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence. (see item 11 below) |
| 11 | Use of <220> | Sequence(s) ____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of Sequence Rules |
| 12 | PatentIn 2.0
"bug" | Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk. |
| 13 | Misuse of n/Xaa | "n" can only represent a single <u>nucleotide</u> ; "Xaa" can only represent a single <u>amino acid</u> |



IFWP

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/594,732

DATE: 10/10/2006

TIME: 15:11:16

Input Set : A:\PTO.KD.txt

Output Set: N:\CRF4\10102006\J594732.raw

3 <110> APPLICANT: NIPPON SHOKUBAI CO., LTD.
 4 NATIONAL INSTITUTE OF TECHNOLOGY AND EVALUATION
 6 <120> TITLE OF INVENTION: Novel Modified S-Hydroxynitrile lyase
 8 <130> FILE REFERENCE: PH-2387-PCT
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/594,732
 C--> 11 <141> CURRENT FILING DATE: 2006-09-29
 13 <150> PRIOR APPLICATION NUMBER: JP 2004-105642
 14 <151> PRIOR FILING DATE: 2004-03-31
 16 <160> NUMBER OF SEQ ID NOS: 44
 18 <170> SOFTWARE: PatentIn Ver. 2.1
 20 <210> SEQ ID NO: 1
 21 <211> LENGTH: 777
 22 <212> TYPE: DNA
 23 <213> ORGANISM: Manihot esculenta
 25 <220> FEATURE:
 26 <223> OTHER INFORMATION: Inventor: Ichige, Eita; Semba, Hisashi; Shijuku, Toshiaki;
 Harayama,
 27 Shigeaki
 29 <220> FEATURE:
 30 <221> NAME/KEY: CDS
 31 <222> LOCATION: (1)..(777)
 33 <400> SEQUENCE: 1
 34 atg gtt act gca cac ttc gtt ctg att cac acc att tgt cac ggc gca 48
 35 Met Val Thr Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala
 36 1 5 10 15
 38 tgg att tgg cac aaa ctg aaa ccg gcc ctg gaa cgt gct ggc cac aaa 96
 39 Trp Ile Trp His Lys Leu Lys Pro Ala Leu Glu Arg Ala Gly His Lys
 40 20 25 30
 42 gtt act gca ctg gac atg gca gcc agt ggc att gac ccg cgt caa att 144
 43 Val Thr Ala Leu Asp Met Ala Ala Ser Gly Ile Asp Pro Arg Gln Ile
 44 35 40 45
 46 gaa cag atc aac tct ttc gat gaa tac tct gaa ccg ctg ctg act ttc 192
 47 Glu Gln Ile Asn Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe
 48 50 55 60
 50 ctg gaa aaa ctg ccg caa ggc gaa aag gtt atc att gtt ggt gaa agc 240
 51 Leu Glu Lys Leu Pro Gln Gly Glu Lys Val Ile Ile Val Gly Glu Ser
 52 65 70 75 80
 54 tgt gca ggc ctg aac att gct att gct gct gat cgt tac gtt gac aaa 288
 55 Cys Ala Gly Leu Asn Ile Ala Ile Ala Ala Asp Arg Tyr Val Asp Lys
 56 85 90 95
 58 att gca gct ggc gtt ttc cac aac tcc ctg ctg ccg gac acc gtt cac 336
 59 Ile Ala Ala Gly Val Phe His Asn Ser Leu Leu Pro Asp Thr Val His
 60 100 105 110
 62 agc ccg tct tac act gtt gaa aag ctg ctg gaa tcg ttc ccg gac tgg 384

*See item 4
on Error Summary
Sheet*

**Does Not Comply
Corrected Diskette Needed**

see pp 6-8

RAW SEQUENCE LISTING

DATE: 10/10/2006

PATENT APPLICATION: US/10/594,732

TIME: 15:11:16

Input Set : A:\PTO.KD.txt

Output Set: N:\CRF4\10102006\J594732.raw

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63 Ser Pro Ser Tyr Thr Val Glu Lys Leu Leu Glu Ser Phe Pro Asp Trp
64      115      120      125
66 cgt gac aca gaa tat ttc acg ttc acc aac atc act ggc gaa acc atc 432
67 Arg Asp Thr Glu Tyr Phe Thr Phe Thr Asn Ile Thr Gly Glu Thr Ile
68      130      135      140
70 act acc atg aaa ctg ggt ttc gtt ctg ctg cgt gaa aac ctg ttc acc 480
71 Thr Thr Met Lys Leu Gly Phe Val Leu Leu Arg Glu Asn Leu Phe Thr
72 145      150      155      160
74 aaa tgc act gat ggc gaa tat gaa ctg gca aaa atg gtt atg cgc aag 528
75 Lys Cys Thr Asp Gly Glu Tyr Glu Leu Ala Lys Met Val Met Arg Lys
76      165      170      175
78 ggc tct ctg ttc caa aac gtt ctg gct cag cgt ccg aag ttc act gaa 576
79 Gly Ser Leu Phe Gln Asn Val Leu Ala Gln Arg Pro Lys Phe Thr Glu
80      180      185      190
82 aaa ggc tac ggc tct atc aag aaa gtt tat att tgg acc gat caa gac 624
83 Lys Gly Tyr Gly Ser Ile Lys Lys Val Tyr Ile Trp Thr Asp Gln Asp
84      195      200      205
86 aaa ata ttc ctg ccg gac ttc caa cgc tgg caa att gca aac tac aaa 672
87 Lys Ile Phe Leu Pro Asp Phe Gln Arg Trp Gln Ile Ala Asn Tyr Lys
88      210      215      220
90 ccg gac aag gtt tat cag gtt caa ggc ggc gat cac aag ctg cag ctg 720
91 Pro Asp Lys Val Tyr Gln Val Gln Gly Gly Asp His Lys Leu Gln Leu
92 225      230      235      240
94 aca aaa act gaa gaa gta gct cac att ctg caa gaa gtt gct gat gca 768
95 Thr Lys Thr Glu Glu Val Ala His Ile Leu Gln Glu Val Ala Asp Ala
96      245      250      255
98 tac gct taa 777
99 Tyr Ala
102 <210> SEQ ID NO: 2
103 <211> LENGTH: 258
104 <212> TYPE: PRT
105 <213> ORGANISM: Manihot esculenta
107 <400> SEQUENCE: 2
108 Met Val Thr Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala
109 1      5      10      15
110 Trp Ile Trp His Lys Leu Lys Pro Ala Leu Glu Arg Ala Gly His Lys
111      20      25      30
112 Val Thr Ala Leu Asp Met Ala Ala Ser Gly Ile Asp Pro Arg Gln Ile
113      35      40      45
114 Glu Gln Ile Asn Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe
115      50      55      60
116 Leu Glu Lys Leu Pro Gln Gly Glu Lys Val Ile Ile Val Gly Glu Ser
117 65      70      75      80
118 Cys Ala Gly Leu Asn Ile Ala Ile Ala Ala Asp Arg Tyr Val Asp Lys
119      85      90      95
120 Ile Ala Ala Gly Val Phe His Asn Ser Leu Leu Pro Asp Thr Val His
121      100      105      110
122 Ser Pro Ser Tyr Thr Val Glu Lys Leu Leu Glu Ser Phe Pro Asp Trp
123      115      120      125

```

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/594,732

DATE: 10/10/2006

TIME: 15:11:16

Input Set : A:\PTO.KD.txt

Output Set: N:\CRF4\10102006\J594732.raw

```

124 Arg Asp Thr Glu Tyr Phe Thr Phe Thr Asn Ile Thr Gly Glu Thr Ile
125      130      135      140
126 Thr Thr Met Lys Leu Gly Phe Val Leu Leu Arg Glu Asn Leu Phe Thr
127 145      150      155      160
128 Lys Cys Thr Asp Gly Glu Tyr Glu Leu Ala Lys Met Val Met Arg Lys
129      165      170      175
130 Gly Ser Leu Phe Gln Asn Val Leu Ala Gln Arg Pro Lys Phe Thr Glu
131      180      185      190
132 Lys Gly Tyr Gly Ser Ile Lys Lys Val Tyr Ile Trp Thr Asp Gln Asp
133      195      200      205
134 Lys Ile Phe Leu Pro Asp Phe Gln Arg Trp Gln Ile Ala Asn Tyr Lys
135      210      215      220
136 Pro Asp Lys Val Tyr Gln Val Gln Gly Gly Asp His Lys Leu Gln Leu
137 225      230      235      240
138 Thr Lys Thr Glu Glu Val Ala His Ile Leu Gln Glu Val Ala Asp Ala
139      245      250      255
140 Tyr Ala
144 <210> SEQ ID NO: 3
145 <211> LENGTH: 774
146 <212> TYPE: DNA
147 <213> ORGANISM: Hevea brasiliensis
149 <220> FEATURE:
150 <221> NAME/KEY: CDS
151 <222> LOCATION: (1)..(774)
153 <400> SEQUENCE: 3
154 atg gca ttc gct cat ttt gtt ctt att cat acc ata tgc cac ggt gca 48
155 Met Ala Phe Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala
156 1      5      10      15
158 tgg att tgg cac aag ctc aaa ccc ctc ctt gag gca ctt ggc cac aag 96
159 Trp Ile Trp His Lys Leu Lys Pro Leu Leu Glu Ala Leu Gly His Lys
160      20      25      30
162 gtt act gca ctg gac ctt gca gca agc ggc gtt gac cca agg caa att 144
163 Val Thr Ala Leu Asp Leu Ala Ala Ser Gly Val Asp Pro Arg Gln Ile
164      35      40      45
166 gag gag att ggc tca ttt gat gag tat tct gaa ccc ttg ttg acg ttc 192
167 Glu Glu Ile Gly Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe
168      50      55      60
170 ttg gag gca ctc cct cca ggg gaa aag gtg att ctg gtt ggc gag agc 240
171 Leu Glu Ala Leu Pro Pro Gly Glu Lys Val Ile Leu Val Gly Glu Ser
172 65      70      75      80
174 tgt gga gga ctc aat ata gca att gct gct gat aaa tac tgt gaa aag 288
175 Cys Gly Gly Leu Asn Ile Ala Ile Ala Ala Asp Lys Tyr Cys Glu Lys
176      85      90      95
178 att gca gct gct gtt ttc cac aat tca gta ttg cca gac acc gag cac 336
179 Ile Ala Ala Ala Val Phe His Asn Ser Val Leu Pro Asp Thr Glu His
180      100      105      110
182 tgc cca tct tac gtc gtg gat aag ctc atg gag gtg ttt ccc gac tgg 384
183 Cys Pro Ser Tyr Val Val Asp Lys Leu Met Glu Val Phe Pro Asp Trp
184      115      120      125

```

RAW SEQUENCE LISTING

DATE: 10/10/2006

PATENT APPLICATION: US/10/594,732

TIME: 15:11:16

Input Set : A:\PTO.KD.txt

Output Set: N:\CRF4\10102006\J594732.raw

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186 aaa gac acc acg tat ttt acg tac act aaa gat ggc aag gag ata act 432
187 Lys Asp Thr Thr Tyr Phe Thr Tyr Thr Lys Asp Gly Lys Glu Ile Thr
188 130 135 140
190 gga ttg aaa ctg ggc ttc acg ctt ctg agg gaa aat tta tat acc ctt 480
191 Gly Leu Lys Leu Gly Phe Thr Leu Leu Arg Glu Asn Leu Tyr Thr Leu
192 145 150 155 160
194 tgc ggt cct gag gaa tat gaa ctg gcg aag atg ttg aca agg aag gga 528
195 Cys Gly Pro Glu Glu Tyr Glu Leu Ala Lys Met Leu Thr Arg Lys Gly
196 165 170 175
198 tca tta ttt caa aat att tta gct aag cga cca ttc ttc act aag gaa 576
199 Ser Leu Phe Gln Asn Ile Leu Ala Lys Arg Pro Phe Phe Thr Lys Glu
200 180 185 190
202 ggt tac gga tcg att aag aaa att tat gtg tgg acc gac caa gac gaa 624
203 Gly Tyr Gly Ser Ile Lys Lys Ile Tyr Val Trp Thr Asp Gln Asp Glu
204 195 200 205
206 ata ttt tta cct gaa ttt caa ctc tgg caa ata gaa aac tat aaa cca 672
207 Ile Phe Leu Pro Glu Phe Gln Leu Trp Gln Ile Glu Asn Tyr Lys Pro
208 210 215 220
210 gac aag gtt tat aag gtc gaa ggt gga gat cat aaa ttg cag ctt aca 720
211 Asp Lys Val Tyr Lys Val Glu Gly Gly Asp His Lys Leu Gln Leu Thr
212 225 230 235 240
214 aag act aag gag atc gct gaa att ctc caa gag gtg gct gat acc tat 768
215 Lys Thr Lys Glu Ile Ala Glu Ile Leu Gln Glu Val Ala Asp Thr Tyr
216 245 250 255
218 aat tga 774
219 Asn
222 <210> SEQ ID NO: 4
223 <211> LENGTH: 257
224 <212> TYPE: PRT
225 <213> ORGANISM: Hevea brasiliensis
227 <400> SEQUENCE: 4
228 Met Ala Phe Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala
229 1 5 10 15
230 Trp Ile Trp His Lys Leu Lys Pro Leu Leu Glu Ala Leu Gly His Lys
231 20 25 30
232 Val Thr Ala Leu Asp Leu Ala Ala Ser Gly Val Asp Pro Arg Gln Ile
233 35 40 45
234 Glu Glu Ile Gly Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe
235 50 55 60
236 Leu Glu Ala Leu Pro Pro Gly Glu Lys Val Ile Leu Val Gly Glu Ser
237 65 70 75 80
238 Cys Gly Gly Leu Asn Ile Ala Ile Ala Ala Asp Lys Tyr Cys Glu Lys
239 85 90 95
240 Ile Ala Ala Ala Val Phe His Asn Ser Val Leu Pro Asp Thr Glu His
241 100 105 110
242 Cys Pro Ser Tyr Val Val Asp Lys Leu Met Glu Val Phe Pro Asp Trp
243 115 120 125
244 Lys Asp Thr Thr Tyr Phe Thr Tyr Thr Lys Asp Gly Lys Glu Ile Thr
245 130 135 140

```

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/594,732

DATE: 10/10/2006

TIME: 15:11:16

Input Set : A:\PTO.KD.txt

Output Set: N:\CRF4\10102006\J594732.raw

```

246 Gly Leu Lys Leu Gly Phe Thr Leu Leu Arg Glu Asn Leu Tyr Thr Leu
247 145 150 155 160
248 Cys Gly Pro Glu Glu Tyr Glu Leu Ala Lys Met Leu Thr Arg Lys Gly
249 165 170 175
250 Ser Leu Phe Gln Asn Ile Leu Ala Lys Arg Pro Phe Phe Thr Lys Glu
251 180 185 190
252 Gly Tyr Gly Ser Ile Lys Lys Ile Tyr Val Trp Thr Asp Gln Asp Glu
253 195 200 205
254 Ile Phe Leu Pro Glu Phe Gln Leu Trp Gln Ile Glu Asn Tyr Lys Pro
255 210 215 220
256 Asp Lys Val Tyr Lys Val Glu Gly Gly Asp His Lys Leu Gln Leu Thr
257 225 230 235 240
258 Lys Thr Lys Glu Ile Ala Glu Ile Leu Gln Glu Val Ala Asp Thr Tyr
259 245 250 255
260 Asn
264 <210> SEQ ID NO: 5
265 <211> LENGTH: 777
266 <212> TYPE: DNA
267 <213> ORGANISM: Manihot esculenta
269 <220> FEATURE:
270 <223> OTHER INFORMATION: cDNA coding for Modified SHNL involving
271 a replacement of Gly by Asp at position 165
273 <220> FEATURE:
274 <221> NAME/KEY: CDS
275 <222> LOCATION: (1)..(777)
277 <400> SEQUENCE: 5
278 atg gtt act gca cac ttc gtt ctg att cac acc att tgt cac ggc gca 48
279 Met Val Thr Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala
280 1 5 10 15
282 tgg att tgg cac aaa ctg aaa ccg gcc ctg gaa cgt gct ggc cac aaa 96
283 Trp Ile Trp His Lys Leu Lys Pro Ala Leu Glu Arg Ala Gly His Lys
284 20 25 30
286 gtt act gca ctg gac atg gca gcc agt ggc att gac ccg cgt caa att 144
287 Val Thr Ala Leu Asp Met Ala Ala Ser Gly Ile Asp Pro Arg Gln Ile
288 35 40 45
290 gaa cag atc aac tct ttc gat gaa tac tct gaa ccg ctg ctg act ttc 192
291 Glu Gln Ile Asn Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe
292 50 55 60
294 ctg gaa aaa ctg ccg caa ggc gaa aag gtt atc att gtt ggt gaa agc 240
295 Leu Glu Lys Leu Pro Gln Gly Glu Lys Val Ile Ile Val Gly Glu Ser
296 65 70 75 80
298 tgt gca ggc ctg aac att gct att gct gct gat cgt tac gtt gac aaa 288
299 Cys Ala Gly Leu Asn Ile Ala Ile Ala Ala Asp Arg Tyr Val Asp Lys
300 85 90 95
302 att gca gct ggc gtt ttc cac aac tcc ctg ctg ccg gac acc gtt cac 336
303 Ile Ala Ala Gly Val Phe His Asn Ser Leu Leu Pro Asp Thr Val His
304 100 105 110
306 agc ccg tct tac act gtt gaa aag ctg ctg gaa tcg ttc ccg gac tgg 384
307 Ser Pro Ser Tyr Thr Val Glu Lys Leu Leu Glu Ser Phe Pro Asp Trp

```

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<210> 17
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 17
ggcgaatatg aactggcaaa aatg^onnnatg cgcaagggct ctctg

45

*These need explanation
(see p. 7)*

subsequent sequences also show this error

VARIABLE LOCATION SUMMARY

DATE: 10/10/2006

PATENT APPLICATION: US/10/594,732

TIME: 15:11:17

Input Set : A:\PTO.KD.txt

Output Set: N:\CRF4\10102006\J594732.raw

error explanation

Use of n's or Xaa's (NEW RULES):

Use of n's and/or Xaa's have been detected in the Sequence Listing.

Use of <220> to <223> is MANDATORY if n's or Xaa's are present.

in <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

Seq#:17; N Pos. 25,26,27

Seq#:18; N Pos. 19,20,21

Seq#:23; N Pos. 19,20,21

Seq#:24; N Pos. 19,20,21

Seq#:37; N Pos. 23,24,25

Seq#:38; N Pos. 21,22,23

see p. 8

10/594,732 8

Tyr Ala

1/49 delete at end of file (after sequence 44)

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/594,732

DATE: 10/10/2006

TIME: 15:11:17

Input Set : A:\PTO.KD.txt

Output Set: N:\CRF4\10102006\J594732.raw

L:10 M:270 C: Current Application Number differs, Replaced Application Number
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:729 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:17
L:729 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:17
L:729 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17 after pos.:0
L:741 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:18
L:741 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:18
L:741 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18 after pos.:0
L:1009 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:23
L:1009 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:23
L:1009 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23 after pos.:0
L:1021 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:24
L:1021 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:24
L:1021 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24 after pos.:0
L:1698 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:37
L:1698 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:37
L:1698 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:0
L:1710 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:38
L:1710 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:38
L:1710 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:38 after pos.:0
L:1727 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:39,Line#:1725
L:1890 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:41,Line#:1888
L:2053 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:43,Line#:2051